



## Enhancing Bacteria Classification using Image Processing and Convolutional Neural Network



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### ABSTRACT

Bacteria classification plays a vital role in the medical field, facilitating the diagnosis and treatment of various diseases. Traditionally, clinical specialists have relied on conventional techniques for classification, which lack predictive capabilities. Manual classification of bacteria is a laborious and time-consuming task that demands significant human effort. However, advancements in technology have opened possibilities for microorganism classification through the utilization of novel machine learning algorithms. This research explores the integration of Convolutional Neural Networks (CNNs) for the classification of bacterial samples, aiming to revolutionize the traditional manual classification methods in the medical field. The methodology involves three stages: image acquisition, feature extraction, and classification. Employing the Enhanced CNN model, the study demonstrates the effectiveness of deep learning techniques in image classification on a diverse bacterial species. Experimental results reveal superior accuracy compared to existing baseline methods, showcasing the potential of deep learning for efficient and precise bacteria classification. The proposed approach has the potential to alleviate the manual classification burden, saving time, and reducing dependence on human expertise. This research contributes to advancing healthcare practices by enhancing the accuracy and precision of 95% and 93.2% respectively for bacterial classification.

### Keywords:

Bacteria classification,  
Deep learning,  
Convolutional Neural Networks (CNNs),  
ResNet-50,  
Image classification,  
Medical diagnosis.

### INTRODUCTION

Bacterial classification stands as a pivotal element in the medical domain, crucial for precise diagnoses and effective disease treatments. Traditionally, clinical specialists have navigated through conventional techniques that, regrettably, lack predictive capabilities (Mohammed & Benlamri, 2014). The manual classification of bacteria, a labor-intensive endeavor, demands substantial human effort, as noted in (Butploy et al., 2021). Recent technological strides, however, have ushered in a new era for microorganism classification, harnessing the potential in Machine learning (ML) algorithms (Panicker et al., 2018). ML, Deep learning (DL) and Transfer learning (TL) are subsets of larger domain of Artificial Intelligence (AI) deployed in all aspect of human existence. Among these, Convolutional Neural Networks (CNNs), have emerged as promising contenders for image classification in various fields (Holmström et al., 2017; Peixinho et al., 2016).

This study builds on the foundation aiming to revolutionize bacteria classification through the synergy of image processing techniques and deep learning

methodologies. Our proposed approach unfolds across three pivotal stages: image acquisition, feature extraction, and classification. Initial microscopic imaging captures the morphological characteristics of bacterial samples. Subsequently, a suite of image processing techniques, including noise reduction, contrast enhancement, and image segmentation, is applied to elevate the quality of the acquired images.

Deep learning models, notably the ResNet-50 CNN model, are employed for feature extraction and subsequent classification. Recognized for their success in diverse image recognition tasks, CNNs, with their capacity to autonomously discern discriminative features, prove particularly well-suited for bacteria classification.

The efficacy of our proposed approach will be rigorously examined through experiments conducted on a dataset comprising of two bacterial species. Results are anticipated to underscore the effectiveness of image processing techniques in augmenting image quality, subsequently elevating classification performance. The ResNet-50 CNN model is poised to demonstrate high accuracy, surpassing existing methods and emphasizing

the transformative potential of deep learning in bacteria classification.

This research's anticipated benefits are profound, seeking to alleviate the labor-intensive manual classification burden, save time, and reduce dependence on human expertise. By leveraging CNNs and integrating advanced image processing techniques, our approach promises to enhance the accuracy and efficiency of bacteria classification, thereby advancing medical diagnoses and treatments. In essence, this study represents a significant leap forward, bridging the gap between conventional methodologies and cutting-edge technology. The expected experimental results will affirm the superiority of our proposed technique, establishing it as an asset for bacteria classification in the medical field.

### Related Work

In the evolving landscape of medical image analysis, machine learning (ML) techniques, particularly Deep Learning (DL) algorithms, have demonstrated remarkable potential and efficiency in the classification of microscopic images for various medical applications. This literature review explores the progression in the widespread adoption of Convolutional Neural Networks (CNNs) in the domain of bacterial species classification. The study by Rujichan et al. (2019) investigated the use of convolutional neural networks (CNNs) for bacterial species classification, emphasizing the robustness and effectiveness of their approach in microbial classification. Their findings demonstrated high accuracy in predicting bacteria species, regardless of image resolution, and explored the impact of varying epochs and activation functions on model performance.

Similarly, A novel automated model which quickly detects and classifies live bacteria in water by using deep neural networks to analyze holographic images was proposed by (Wang et al., 2020). (Li et al., 2022) proposed a model that incorporates a lens-free imaging modality and employs two deep neural networks to detect, count, and identify bacterial colonies. The system demonstrated high efficacy when tested with various coliform bacteria, achieving an average CFU detection rate of 97.3% at 9 hours of incubation and an average recovery rate of 91.6% at approximately 12 hours.

In a related work in (Butploy et al., 2021) proposed a deep learning approach for classifying *A. lumbricoides* eggs using CNN, achieving high accuracy through the optimization of CNN architecture with different convolution layers and tuning parameters. Their model proved effective in reducing manual image classification effort, showcasing potential applications in parasitic egg classification.

The work of (Dacal et al., 2021) presented a system using smartphones and deep learning algorithms to detect and count soil-transmitted helminth (STH) eggs in digitized microscopy images. Their work demonstrated the

integration of smartphone-assisted microscopy for remote analysis, providing a potential solution for improving accessibility and quality of STH diagnosis in low-resource settings.

Kumar et al. (2023) introduced a YOLOv5-based deep learning model for detecting and classifying intestinal parasite eggs from microscopic images, outperforming other methods, and demonstrating its potential for real-time diagnosis and treatment of parasitic infections. The model incorporated data augmentation techniques to enhance dataset diversity.

In a different context, Suwannaphong et al. (2023) employed transfer learning for automatic parasite egg detection and classification during fecal examinations. Their proposed ResNet50 framework exhibited high accuracy in classifying parasitic eggs, even in low-quality images from a USB microscope. This approach showcased robustness in handling diverse data, suggesting its applicability in real fecal examinations using USB microscopes.

AIDahoul et al. (2023) adds another dimension to the related work, showcasing a highly accurate technique called Convolution and Attention Networks (CoAtNet) for automated recognition and classification of 11 types of parasite eggs from microscopic images. The study demonstrates the superiority of the CoAtNet model over other deep learning approaches, including CNNs and vision transformers, with an impressive average accuracy and F1 score of 93%. The CoAtNet model combines the strengths of convolutional networks and vision transformers to automatically extract informative features, enhancing the differentiation of parasite egg categories. The tuning of all layers in CoAtNet allows it to learn parameters specific to the parasitic egg image classification task.

Moreover, AIDahoul et al.'s proposed approach has the potential to reduce errors, improve sensitivity, and integrate seamlessly into parasitological diagnosis systems for identifying common protozoan and helminth infections, particularly in low-income countries. However, the study acknowledges limitations, such as increased computational costs for tuning all layers and the inability to localize multiple eggs. Nevertheless, the overall contribution of this study is significant, presenting a highly accurate deep learning solution for automated parasitic egg recognition that can greatly assist in microscopy-based diagnosis.

The literature presents recent advancements in deep learning applications for microbial and parasitic detection and classification. It examined species classification's robustness regardless of image resolution (Chavis et al. 2019), automated models for live detection and identification of bacteria (Wang et al., 2020; Li et al., 2022), labour cost reduction in *A. lumbricoides* eggs classification (Butploy et al., 2021), solution for improved accessibility in low-resource settings (Elena et

al., 2021), intestinal parasite eggs detection (Kumar et al., 2023), transfer learning for automated parasite egg detection (Suwannaphong et al., 2023) and CoAtNet, an automated recognition and classification of 11 types of parasite eggs (AlDahoul et al., 2023).

However, despite the promised potential of the examined literature, existing solutions for automated recognition of parasite eggs in microscopic images, such as (Butploy et al., 2021 and AlDahoul et al., 2023), still need improvements to reduce diagnostic errors and generate fast, efficient, and accurate results. In this research, we aimed to build an enhanced CNN model that can classify two species of intestinal parasite with improve accuracy and precision compared to the baseline studies. Overall, our approach is expected to contribute to the advancement of deep learning solutions for automated microbial and parasitic detection, offering promising prospects for diagnosis and treatment.

In summary, the review demonstrated a widespread adoption of Convolutional Neural Networks (CNNs) for bacterial species classification. The findings collectively underscore the potential and advancements in medical image analysis, paving the way for more sophisticated and accurate diagnostic tools in microbiology.

## MATERIALS AND METHODS

In this section, the dataset and the different stages involved in developing the model are outlined and examined. The parasite images were collected as an input data from General Hospital Funtua in Katsina state Nigeria. For both types of the intestinal parasites, *Ascaris Lumbricoides* ova (ALO) and *Trichuris trichiura* ova (TTO), 300 images were obtained for the experiment. Fig. 1 depicts the different phases of the method adopted in developing, training and evaluation of the model.

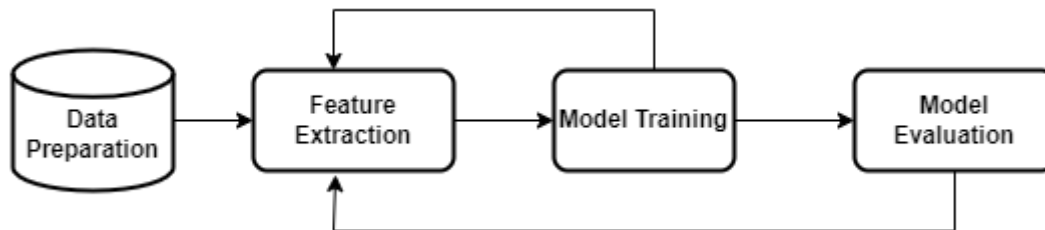


Figure 1: Different stages of model development process

### Data Preparation

#### Collection and Cleansing

The dataset preparation involved the collection of parasite images sourced from General Hospital Funtua, Katsina, Nigeria. The collection process utilized a microscope equipped with a digital camera, connected to a PC through specialized software. Specifically, 100 images were gathered for each of the two types of parasites, *Ascaris lumbricoides* ova (ALO) and *Trichuris trichiura*

ova (TTO). Following this data acquisition, the dataset underwent a meticulous two-step preparation: firstly, a careful assortment of microscopic bacteria images, ensuring a representative and diverse selection, and secondly, pre-processing procedures such as noise reduction and image normalization to enhance the overall quality and suitability of the dataset for subsequent analysis for machine learning applications. Fig 2a and b illustrate sample images.

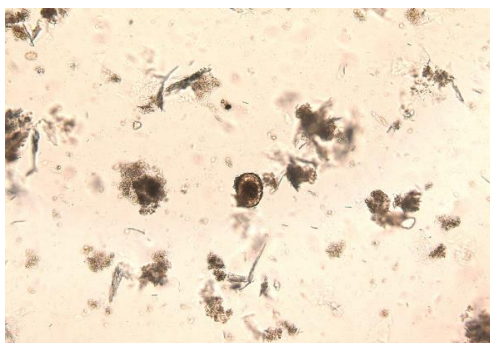


Figure 2(a) : *Ascaris Lumbricoides* Ova (ALO)

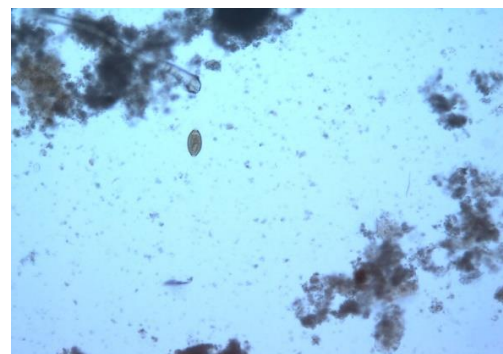


Figure 2(b): *Trichuris Trichiura* Ova (TTO)

**Image Augmentation**

Image Augmentation played a pivotal role in augmenting the dataset by increasing the quantity of image data, particularly when the available data were deemed insufficient for diverse transformations. Various techniques were employed to introduce diversity and variability into the dataset, including rotation, zooming in/out, and reflection. These augmentation methods contribute not only to expanding the dataset but also to enhancing the robustness of machine learning models by exposing them to a broader range of visual scenarios. The dataset is limited, hence the need for augmentation. Training a Convolutional Neural Network (CNN) on smaller datasets increases the susceptibility to overfitting. This impedes CNN's capacity to effectively generalize to unseen and invariant data.

**Model development**

The Convolutional Neural Network (CNN) architecture deployed in this study is meticulously crafted to proficiently process and discern intricate features within the dataset. The model's configuration is characterized by a sequence of key layers that collectively contribute to its robust analytical capabilities. At the forefront of the architecture is the *Conv2D* layer, a pivotal element for feature extraction. Employing 32 filters of dimensions 3 by 3, this layer systematically traverses the input images, capturing nuanced patterns and spatial information crucial for subsequent classification endeavours. Fig 3 represents a 2D convolutional layer

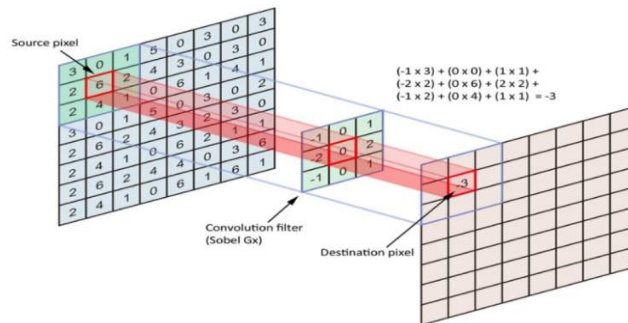


Figure 3: Convolutional 2D layer

After the convolutional layer, the *MaxPooling2D* layer is strategically introduced to down sample the spatial dimensions of the acquired features. This reduction not only alleviates computational complexity but also accentuates salient features by effectively halving the size of the images. The ensuing Flatten layer assumes a central role, orchestrating the transformation of processed images from a 2D array to a 1D array. This pivotal step optimally readies the data for seamless integration into

the subsequent dense layers of the neural network, facilitating a streamlined flow of information. The *Fully-Connected* layer establishes connections between the neurons in one layer and all the nodes in the subsequent layers, enabling the computation of weights and biases derived from the preceding layer. Consequently, during the backpropagation process in the Fully Connected layer, the model iteratively refines and adjusts the weights and biases, facilitating the fine-tuning of the neural network.

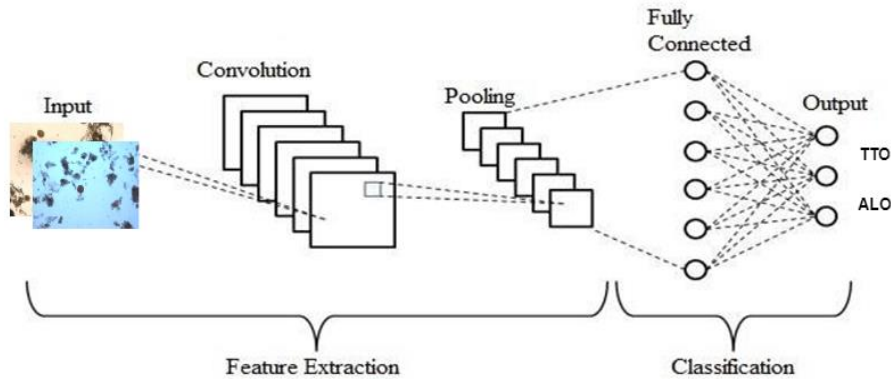


Figure 4: CNN architecture, integrating convolutional, pooling, flattening, and dense layers

To introduce essential non-linearity, the *Relu* (Rectified Linear Unit) activation function is judiciously applied. Its role is paramount in ensuring that negative values are rectified to zero, endowing the model with the capacity to discern intricate relationships inherent in the data. Culminating the model architecture is the *Softmax* layer, comprising 6 neurons, each dedicated to representing a distinct class. Employing the *Softmax* activation function, this layer computes probabilities for the input image's association with predefined classes. This configuration, tailored for multi-class classification, underscores its suitability for intricate categorization challenges. Fig 3 depicts the different layers in the architecture.

In essence, the holistic CNN architecture, integrating convolutional, pooling, flattening, and fully connected layers, stands as a testament to its efficacy in processing and classifying diverse features within the dataset, thereby establishing a foundation for precise and insightful image classification. Fig 4 depicts the CNN architecture.

**RESULTS AND DISCUSSION**

In the experiment, Google collab was used. Dataset was divided into 40% for training, 30% for testing and 30% for validation. Augmentation was done to increase the dataset size. The model architecture is designed in a sequential manner for effective image classification. It begins with a Conv2D layer using 32 filters of size 3 by 3, extracting intricate features from input images. A subsequent MaxPooling2D layer reduces spatial dimensions, retaining vital information while minimizing computational complexity.

The Flatten layer transforms the 2D-array image representation into a 1D-array, facilitating integration with densely connected layers. Rectified Linear Unit (ReLU) activation introduces non-linearity, enhancing the model's capacity to learn complex patterns. The final layer employs Sigmoid activation with 2 neurons for binary classification probabilities. Training occurs in batches of 128 samples with *Adam* as optimizer and learning rate at 0.0001 optimizing computational efficiency, and spans 20 epochs for comprehensive learning and parameter adjustment. Fig 5a show the disparity between training accuracy and loss.

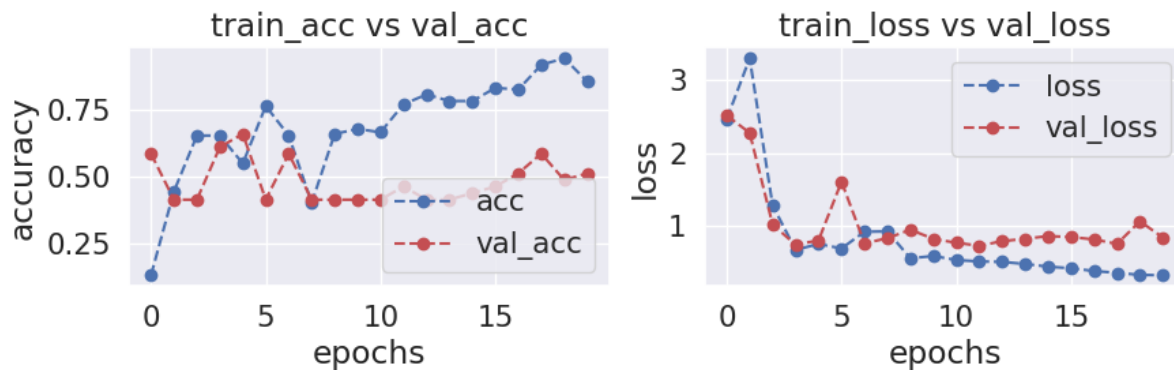


Figure 5: shows the *accuracy* learning rate in left hand side and *loss* training rate on the right hand side

**Model Evaluation**

To evaluate the robustness of the experiments conducted on the trained Convolutional Neural Network (CNN) model, we employ metrics such as Precision, Recall, F1-score, and mean Average Precision (mAP) for evaluation purposes. The computation procedures for these metrics are elucidated in equations 1 through 3

$$Recall = \frac{TP}{TP+FP} \tag{1}$$

$$Precision = \frac{TP}{TP+FN} \tag{2}$$

$$F1 - Score = 2 * \frac{Precision * Recall}{Precision + Recall} \tag{3}$$

In this context, the notations TP, TN, FN, and FP denote True Positive (indicating correct detections), True Negative, False Positive (reflecting incorrect detections), and False Negative (representing missed detections). The F1-score metric serves to elucidate the balance between Recall and Precision, providing a comprehensive

assessment of the trained model's performance, as articulated in equation (3).

**Comparison with Previous work**

To contextualize our findings, we conducted a comparative analysis with existing research within the domain, specifically examining the outcomes reported by Butploy et al. in 2021 and Aldahoul et al. in 2023. The comparative results are meticulously presented in Table 1. Notably, our proposed deep learning model demonstrates a remarkable total accuracy of 95%, surpassing the baseline accuracy observed in prior studies. This noteworthy improvement indicates the heightened efficacy of our model in identifying and classifying *A. lumbricoides* and *T. trichiura*, underscoring its enhanced performance in relation to established benchmarks.

**Table 1: Comparison with existing studies**

| Authors                | Methods              | %Accuracy | %Precision | %Recall | %F1 Score |
|------------------------|----------------------|-----------|------------|---------|-----------|
| Butploy et al. (2021)  | CNN                  | 93.3      | 86.6       | 92.8    | 89.6      |
| Aldahoul et al. (2023) | Multi-modal learning | 92.0      | 93.0       | 93.0    | 93.0      |
| Ahmad et al. (2023)    | Enhanced CNN         | 95.0      | 93.2       | 93.8    | 93.5      |

## CONCLUSION

In conclusion, our study substantiates that the cost-effective digital microscope employed herein exhibits commendable imaging capabilities, reliably discerning prevalent helminth parasite classifications, specifically *A. lumbricoides* and *T. trichiura*, within fixated stool samples. Additionally, our investigation introduces a novel dimension by illustrating the efficacy of a deep learning-based image analysis model for automating the detection of helminth parasites in such samples. These findings contribute to the existing body of knowledge, affirming the viability of low-cost digital imaging tools for point-of-care diagnosis in rural settings. Nonetheless, it is imperative to underscore the necessity for further rigorous validations of these techniques prior to their integration into clinical environments.

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